B2 cont.

2. (Amended) The method according to claim 1, wherein the mutated PTKR is a mutated epidermal growth factor receptor (EGFR).

3. (Amended) The method according to claim 2, wherein the mutated EGFR is a mutated EGFR1.

B3

5. (Amended) The method according to claim 1, wherein the mutated PTKR comprises a deletion in the intracellular domain or deletions in both the intracellular domain and the extracellular domain.

6. (Amended) The method according to claim 2, wherein the introducing step is accomplished by incorporating the nucleic acid sequence encoding the mutated EGFR into a vector and introducing said vector into said mammalian cell.

B4

8. (Amended) The method according to claim 1, wherein said identifying step is accomplished by contacting the genetically modified mammalian cells with an antibody that recognizes and binds to the mutated PTKR.

B5

10. (Amended) The method according to claim 1, further comprising separating the identified cells expressing the mutated PTKR.

11. (Amended) The method according to claim 1, wherein the mammalian cells are human cells.

12. (Amended) The method according to claim 11, wherein the human cells are selected from the group consisting of hematopoietic cells, liver cells, endothelial cells and smooth muscle cells.

13. (Amended) The method according to claim 11, wherein the human cells are hematopoietic cells.

14. (Amended) The method according to claim 13, wherein the hematopoietic cells are stem cells or T-cells.

16. (Amended) A method of identifying genetically modified mammalian cells comprising the steps of:

a) incorporating into a vector a nucleic acid sequence encoding a mutated protein-tyrosine kinase receptor (PTKR), wherein said PTKR comprises modifications to the intracellular and the extracellular domains, comprises a modification to the extracellular domain, or excludes any nerve growth factor receptor(s) (NGFR) and comprises a modification to the intracellular domain;

B6

b) introducing the vector into a mammalian cell to form a genetically modified mammalian cell;

c) allowing expression of the mutated PTKR in the genetically modified mammalian cell; and

d) identifying said genetically modified mammalian cell expressing the mutated PTKR.

17. (Amended) The method according to claim 16, wherein the mutated PTKR is a mutated EGFR.

Sub C2

20. (Amended) A method for identifying transduced mammalian cells comprising:

a) retrovirally transducing mammalian cells with a nucleic acid sequence encoding a protein-tyrosine kinase receptor (PTKR) operatively linked to an expression control sequence; wherein said PTKR comprises modifications to the intracellular and the extracellular domains, comprises a modification to the extracellular domain, or excludes any nerve growth factor receptor(s) (NGFR) and comprises a modification to the intracellular domain;

B7

b) incubating the transduced mammalian cells with a marked antibody which recognizes and binds specifically to the mutated PTKR; and

c) identifying the marked transduced mammalian cells.

21. (Amended) The method according to claim 20, wherein the mammalian cells are hematopoietic cells.

22. (Amended) The method according to claim 20, wherein the mutated PTKR is a mutated EGFR.

23. (Amended) The method according to claim 20, wherein the mammalian cells are transduced by a retroviral vector selected from the group consisting of a moloney murine leukemia viral vector, a myeloproliferative sarcoma viral vector, a murine embryonic stem cell viral vector, a murine stem cell viral vector, and a spleen focus forming viral vector.

24. (Amended) The method according to claim 20, wherein the mammalian cells are transduced by a lentiviral vector.

25. (Amended) The method according to claim 20, further comprising the step of separating the identified marked transduced mammalian cells from non-marked mammalian cells.

26. (Amended) The method according to claim 20, further comprising the step of expanding the marked transduced mammalian cells.

27. (Amended) A method of identifying mammalian cells expressing a protein of interest, comprising:

a) introducing into a mammalian cell a nucleic acid comprising a DNA sequence encoding a protein of interest and comprising a DNA sequence encoding a protein-tyrosine kinase receptor (PTKR), wherein said DNA sequences are operatively linked to one or more expression control sequences, wherein said PTKR comprises modifications to the intracellular and the extracellular domains, comprises a modification to the extracellular domain, or excludes any nerve growth factor receptor(s) (NGFR) and comprises a modification to the intracellular domain;

b) culturing the resulting mammalian cells; and

c) identifying mammalian cells which express the mutated PTKR thereby obtaining mammalian cells which express the protein of interest.

28. (Amended) The method according to claim 27, wherein the mutated PTKR is a mutated EGFR.

29. (Amended) The method according to claim 27, wherein the nucleic acid encoding the mutated PTKR and the nucleic acid encoding the protein of interest are introduced by a retroviral vector.

Please add new claims 31-42 as follows:

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31. (New) The method according to claim 3, wherein the mutated EGFR1 comprises the amino acid sequence set forth in SEQ ID NO:2 except that amino acid residues 679-1210 are deleted.

32. (New) The method according to claim 3, wherein the mutated EGFR1 comprises the amino acid sequence set forth in SEQ ID NO:2 except that amino acid residues 25-312 and 679-1210 are deleted.

33. (New) The method according to claim 17, wherein the mutated EGFR is a mutated EGFR1.

34. (New) The method according to claim 33, wherein the mutated EGFR1 comprises the amino acid sequence set forth in SEQ ID NO:2 except that amino acid residues 679-1210 are deleted.

35. (New) The method according to claim 33, wherein the mutated EGFR1 comprises the amino acid sequence set forth in SEQ ID NO:2 except that amino acid residues 25-312 and 679-1210 are deleted.

36. (New) The method according to claim 22, wherein the mutated EGFR is a mutated EGFR1.

37. (New) The method according to claim 36, wherein the mutated EGFR1 comprises the amino acid sequence set forth in SEQ ID NO:2 except that amino acid residues 679-1210 are deleted.

38. (New) The method according to claim 36, wherein the mutated EGFR1 comprises the amino acid sequence set forth in SEQ ID NO:2 except that amino acid residues 25-312 and 679-1210 are deleted.

39. (New) The method according to claim 28, wherein the mutated EGFR is a mutated EGFR1.

40. (New) The method according to claim 39, wherein the mutated EGFR1 comprises the amino acid sequence set forth in SEQ ID NO:2 except that amino acid residues 679-1210 are deleted.

41. (New) The method according to claim 39, wherein the mutated EGFR1 comprises the amino acid sequence set forth in SEQ ID NO:2 except that amino acid residues 25-312 and 679-1210 are deleted.

42. (New) A method of identifying a genetically modified mammalian cell, comprising:

a) introducing a nucleic acid sequence encoding a mutated epidermal growth factor receptor 1 (EGFR1), operatively linked to an expression control sequence, into a mammalian cell to form a genetically modified mammalian cell, wherein the mutated EGFR1 either comprises: i) the amino acid sequence set forth in SEQ ID NO:2 except that amino acid residues 679-1210 are deleted, or ii) the amino acid sequence set forth in SEQ ID NO:2 except that amino acid residues 25-312 and 679-1210 are deleted;

b) allowing expression of the mutated EGFR1 in the genetically modified mammalian cell; and

c) identifying said genetically modified mammalian cell expressing the mutated EGFR1.